FIG. 1A

```
atg tac aac ggg tcg tgc tgc cgc atc gag ggg gac acc atc tcc cag      48
Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
 1               5                  10                  15

gtg atg ccg ccg ctg ctc att gtg gcc ttt gtg ctg ggc gca cta ggc      96
Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
            20                  25                  30

aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag acc tgg aag     144
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
            35                  40                  45

ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat ttc ctc ctt     192
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
        50                  55                  60

atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga cgt aga cac     240
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
65                  70                  75                  80

tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc acg ttg gcc     288
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
                85                  90                  95

atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg gct gcg gac     336
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
            100                 105                 110

agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac act atc tcc     384
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
        115                 120                 125

acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc ctg gtc atc     432
Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
    130                 135                 140

ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc gtg caa gag     480
Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
145                 150                 155                 160

acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc aat ggc tgg     528
Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
                165                 170                 175

cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc ggc atc atc     576
His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
                180                 185                 190

tta ttt tgc tcc ttc aag att gtt tgg agc ctg agg cgg agg cag cag     624
Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
            195                 200                 205
```

```
ctg gcc aga cag gct cgg atg aag aag gcg acc cgg ttc atc atg gtg    672
Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
    210             215             220

gtg gca att gtg ttc atc aca tgc tac ctg ccc agc gtg tct gct aga    720
Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
225             230             235             240

ctc tat ttc ctc tgg acg gtg ccc tcg agt gcc tgc gat ccc tct gtc    768
Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
            245             250             255

cat ggg gcc ctg cac ata acc ctc agc ttc acc tac atg aac agc atg    816
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
            260             265             270

ctg gat ccc ctg gtg tat tat ttt tca agc ccc tcc ttt ccc aaa ttc    864
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
        275             280             285

tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag cca gga cac    912
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
    290             295             300

tca aaa aca caa agg ccg gaa gag atg cca att tcg aac ctc ggt cgc    960
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
305             310             315             320

agg agt tgc atc agt gtg gca aat agt ttc caa agc cag tct gat ggg   1008
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
            325             330             335

caa tgg gat ccc cac att gtt gag tgg cac                           1038
Gln Trp Asp Pro His Ile Val Glu Trp His
            340             345
```

```
gaaaaagaca aaaccagaaa aagaaaagtc atctccaggg ctcgatctag caacgagtct 60

gtagcatgta tagcgtcgga cccccgagct gcaacccaga aatgtacact cgtgggaaac 120

cgcttgcacc ccagagcctg acccagctgc aggcttcaac tctgtagggg acgtgcagct 180

cgtgatccaa gcctaggaga aaggacttgc tgccggcttt catttcctgg ctgaagtttc 240

tctcgtgggt gcagcgcctg catcccaggg tgatgaggtt aggggcccag ctgctagagg 300

agccctagtg ttcggatagg cagctgtgcc tctgtgccgg ccaccttgg atg cca gtc 358
                                                     Met Pro Val
                                                      1
```

```
ctc tct cca act gct atg gac aac ggg tcg tgc tgt ctc atc gag ggg    406
Leu Ser Pro Thr Ala Met Asp Asn Gly Ser Cys Cys Leu Ile Glu Gly
     5               10               15
```

```
gag ccc atc tcc cag gtg atg cct cct cta ctc atc ctg gtc ttc gtg    454
Glu Pro Ile Ser Gln Val Met Pro Pro Leu Leu Ile Leu Val Phe Val
 20               25               30               35
```

```
ctt ggc gcc ctg ggc aac ggc ata gcc ctg tgc ggc ttc tgc ttt cac    502
Leu Gly Ala Leu Gly Asn Gly Ile Ala Leu Cys Gly Phe Cys Phe His
             40               45               50
```

```
atg aag acc tgg aag tca agc act att tac ctt ttc aac ttg gct gtg    550
Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe Asn Leu Ala Val
             55               60               65
```

```
gcc gat ttt ctc ctc atg atc tgc tta ccc ctt cgg aca gac tac tac    598
Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg Thr Asp Tyr Tyr
             70               75               80
```

```
ctc aga cgc aga cac tgg att ttt gga gat atc gcc tgt cgc ctg gtc    646
Leu Arg Arg Arg His Trp Ile Phe Gly Asp Ile Ala Cys Arg Leu Val
     85               90               95
```

```
ctc ttc aag ctg gcc atg aat agg gcc ggg agc att gtc ttc ctc act    694
Leu Phe Lys Leu Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr
100               105               110               115
```

```
gtg gtg gct gtg gat agg tat ttc aaa gtg gtc cac ccc cac cat atg    742
Val Val Ala Val Asp Arg Tyr Phe Lys Val Val His Pro His His Met
             120               125               130
```

```
gtg aat gcc atc tcc aac cgg act gcc gcc gcc acc gcc tgt gtc ctc    790
Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Thr Ala Cys Val Leu
             135               140               145
```

```
tgg act ttg gtc atc ttg ggg act gtg tat ctt ctg atg gag agt cac    838
Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Met Glu Ser His
             150               155               160
```

FIG. 2B

```
ctg tgt gtg cag ggg aca ctg tcg tcc tgt gag agc ttc atc atg gag    886
Leu Cys Val Gln Gly Thr Leu Ser Ser Cys Glu Ser Phe Ile Met Glu
    165             170             175

tca gcc aac ggg tgg cac gat gtc atg ttc cag ctg gag ttc ttc ctg    934
Ser Ala Asn Gly Trp His Asp Val Met Phe Gln Leu Glu Phe Phe Leu
180             185             190             195

ccc ctg aca atc atc ttg ttc tgc tcg gtc aac gtt gtt tgg agc ctg    982
Pro Leu Thr Ile Ile Leu Phe Cys Ser Val Asn Val Val Trp Ser Leu
                200             205             210

aga cgg agg cag cag ctg acc aga cag gct cgg atg agg agg gcc acc   1030
Arg Arg Arg Gln Gln Leu Thr Arg Gln Ala Arg Met Arg Arg Ala Thr
                215             220             225

cgg ttc atc atg gtg gtg gct tct gtg ttc atc acg tgt tac ctg ccc   1078
Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr Cys Tyr Leu Pro
            230             235             240

agc gtg ctg gct agg ctc tac ttc ctc tgg acg gtg ccc act agt gcc   1126
Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro Thr Ser Ala
        245             250             255

tgt gac ccc tct gtc cac aca gcc ctc cac gtc acc ctg agc ttc acc   1174
Cys Asp Pro Ser Val His Thr Ala Leu His Val Thr Leu Ser Phe Thr
260             265             270             275

tac ctg aac agt atg ctg gat ccc ctt gta tat tac ttc tca agc ccc   1222
Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro
                280             285             290

tcg ctc ccc aaa ttc tac gcc aag ctc aca atc tgc agc ctg aag ccc   1270
Ser Leu Pro Lys Phe Tyr Ala Lys Leu Thr Ile Cys Ser Leu Lys Pro
            295             300             305

aaa cgc cca gga cgc acg aag acg cgg agg tca gaa gag atg cca att   1318
Lys Arg Pro Gly Arg Thr Lys Thr Arg Arg Ser Glu Glu Met Pro Ile
        310             315             320

tcg aac ctc tgc agt aag agc tcc atc gat ggg gca aat cgt tcc cag   1366
Ser Asn Leu Cys Ser Lys Ser Ser Ile Asp Gly Ala Asn Arg Ser Gln
        325             330             335

agg cca tct gac ggg cag tgg gat ctc caa gtg tgt tgaatgccat        1412
Arg Pro Ser Asp Gly Gln Trp Asp Leu Gln Val Cys
340             345             350

taagacaaac agcccaacaa cgaggcagag aaatgggcaa tgtgagttaa atctgaaggg 1472

tggaggactt gaagatgtcc cctcccactc ttagctgtat ctttctcact caggtagaaa 1532

tgggatccac cctgcttgac cttttccaga aggttccaaa ccggttggtt gtgtttaaat 1592
```

```
actctgatag caatggtgaa ggggcagcgt gtgagtgtga aggaaaccgt gggtgtcggg 1652

ttaggaacta cctggagccc gtgtcgcttt gcatggctga gaaaagcggt atgagcctgg 1712

ctgggtcttg ttctagctcg gagagagtta acgatctcaa taactcgtcg gtatttcctg 1772

gactgaaaaa aatagaaact gcactgagtc aatacactta tttccagctg agcgagaccc 1832

tttactgcag gacacccgga cctagccgtt tttttaaatc ttccctgggg agcctccaca 1892

catttcaagg tttgaacatc caggtggccc aggagggcag caaaaagaat ctattctaac 1952

cttgctggcg ccacgatatt ttgctgattt taagtggttt catcctttgt ttttcttttg 2012

tttgcatttc aaagaagatg ctgagggact tgtccacctg atatcagcta tcgtttctcc 2072

agtgggaact gagagcctgt ttacggcagc aatggtgggg ggggggtgct tcctggtatt 2132

tgggatgggt taattcaagc atggttgttc ttcactgctt aatgcatgaa tttgagctga 2192

aatcctccct tctcaagtct ttgtttaatc cacagtatgt tgtcccaccc tgtccagcat 2252

cctcgtctgt tttgtctttg gtgctgggca ttgaacttgg gaccttattc gagccaggca 2312

agcactgacc actgaactgc actcccaaac cccttgtgcc ccttttagct gtagcgttgt 2372

tagccaactt ttgggagaaa gcaaagcact agaggtggca gcaacagttt agctcaatgt 2432

cctttcgtca gtgtctagac ttctggtcag ccatccgggt ctcctattgg gggcctccct 2492

caagcacata tgttctccca aatactaccc agaattctca cagctaggtg attctgtgaa 2552

agtccaggct gccctgtcc tggagaagga gaaatagaat ccgtgttaac cttagtccca 2612

ctttcaagcc acaaagtgg tgacagccat tcactctctc cagttcccag ggtactctcc 2672

ccagggaagg gaccttgaca tttatgtcta aagacataaa ttagatgctc ctcaaggttg 2732

tccctgtggc ttcctttgcc agaggtgttg aagcctaggt gcgaaaatca gtctgactgc 2792

agggctggtg agaaggctca gtaggtaaac aggtctgccg ccaagccacc aacctgagta 2852

tccctgagac ccacgtggta ggagaacacc aaatcccaaa ggtggttctg tcctccacct 2912

atgttcacgc atgcgcacat gcacgcatgc gcacgcgcgc acacccaccc accaaataca 2972

ttaatgcaat aaaaatttta ttggctacac ggtcaagttt gaatcttagt ttaaatgctt 3032

attagacatg tgctcgtagg gaagacttta tttaacccca ctcagttttg atgttcagca 3092

gggttaatac tgatgccaaa gggtttggga gcaaattcaa tgactgtaca ctcataagca 3152

tgagaaatct gttgttccca ggtctgcccg gaagaagacc atgtgcgtgt agtagttgat 3212
```

FIG. 2D

```
aaataaatag ttgctgaaca actataatcg ctccaaaaa                    3251
```

FIG. 3A

```
tggtacgcct gcaggtaccg gtccggaatt cccgggtcga cccacgcgtc cgcaaaacta 60

gaaaagcaaa atcgtcccca ggggtggacc cagcgacaag tctgctgcgt ggctggcatc 120

agacccccaa gctgcagcct ggcaatgtac gcttttggaa aactgctctc gcctcagagc 180

ctgacccagc tgcaggcttc acctctgtag gggacatgca gcttgtgatc caggctgagg 240

agaaaggacc tgctgtcggc tttcatttcc tgactgaagt tgggtgatga ggttaggggc 300

ccagctgcca aggggaacca tagtgttcag ataggcagct gtgcctttgt gtcagccacc 360
```

```
tagg atg ctc ttc ctc tct ccg agt gct atg gac aac ggg tcg tgc tgt   409
     Met Leu Phe Leu Ser Pro Ser Ala Met Asp Asn Gly Ser Cys Cys
      1               5                   10                  15

ctc atc gag ggg gaa ccc atc acc cag gta atg cca cct tta ctc atc   457
Leu Ile Glu Gly Glu Pro Ile Thr Gln Val Met Pro Pro Leu Leu Ile
             20                  25                  30

ctg gcc ttc ctg ctt gga gcc ctg ggc aac ggc cta gcc ctg tgt ggt   505
Leu Ala Phe Leu Leu Gly Ala Leu Gly Asn Gly Leu Ala Leu Cys Gly
         35                  40                  45

ttc tgc ttt cac atg aag acc tgg aag tcg agc act att tac ctt ttc   553
Phe Cys Phe His Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe
         50                  55                  60

aac ttg gct gta gcc gat ttt ctc ctc atg atc tgc cta ccc ctt cgg   601
Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg
         65                  70                  75

aca gac tac tac ctc aga cgt agg cat tgg att ttg ggg gat att ccc   649
Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ile Leu Gly Asp Ile Pro
80                  85                  90                  95

tgc cgc ctg gtc ctc ttc atg ctg gcc atg aat agg gcc gga agc att   697
Cys Arg Leu Val Leu Phe Met Leu Ala Met Asn Arg Ala Gly Ser Ile
                 100                 105                 110

gtc ttc ctc act gtg gtg gcc gtg gac agg tat ttc aaa gtg gtc cac   745
Val Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Lys Val Val His
                 115                 120                 125

ccc cac cat atg gtg aac gcc atc tcc aat cgg act gca gct gcc atc   793
Pro His His Met Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Ile
             130                 135                 140

gtc tgt gtc ctc tgg act ttg gtc atc ttg ggg act gtg tat ctt ctg   841
Val Cys Val Leu Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu
         145                 150                 155
```

FIG. 3B

```
atg gag agt cac ctg tgt gtg cgg ggg atg gtg tca tct tgt gag agc      889
Met Glu Ser His Leu Cys Val Arg Gly Met Val Ser Ser Cys Glu Ser
160             165             170             175

ttc atc atg gag tca gcc aac ggg tgg cac gat atc atg ttc cag ctg      937
Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met Phe Gln Leu
            180             185             190

gag ttc ttc ctg ccc ctg acc atc atc ttg ttc tgc tcc ttc aaa gtt      985
Glu Phe Phe Leu Pro Leu Thr Ile Ile Leu Phe Cys Ser Phe Lys Val
        195             200             205

gtt tgg agc ctg aga cag agg caa cag ctg acc aga cag gct cgg atg     1033
Val Trp Ser Leu Arg Gln Arg Gln Gln Leu Thr Arg Gln Ala Arg Met
        210             215             220

agg agg gcc acc cgg ttc atc atg gtg gtg gct tcc gtg ttc atc acg     1081
Arg Arg Ala Thr Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr
    225             230             235

tgt tac ctg ccc agc gtg ttg gcg agg ctc tac ttc ctc tgg acg gtg     1129
Cys Tyr Leu Pro Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val
240             245             250             255

ccc tcc agt gct tgt gac ccc tct gtc cac ata gct ctc cat gtc acc     1177
Pro Ser Ser Ala Cys Asp Pro Ser Val His Ile Ala Leu His Val Thr
            260             265             270

ctg agt ctc acc tac ctg aac agc atg ctg gac cct ctt gtg tac tac     1225
Leu Ser Leu Thr Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr
            275             280             285

ttt tca agc ccc tcg ttc ccc aaa ttc tac gcc aag ctc aaa atc cgc     1273
Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Ala Lys Leu Lys Ile Arg
        290             295             300

agc ttg aaa ccc aga cgc cca gga cgc tcg cag gca cgg agg tcg gaa     1321
Ser Leu Lys Pro Arg Arg Pro Gly Arg Ser Gln Ala Arg Arg Ser Glu
        305             310             315

gag atg cca att tcg aat ctc tgt cgt aag agt tcc acc gat gtg gta     1369
Glu Met Pro Ile Ser Asn Leu Cys Arg Lys Ser Ser Thr Asp Val Val
320             325             330             335

aat agt tcc cag agg ccg tct gac ggg cag tgg ggt ctc caa gtg tgt     1417
Asn Ser Ser Gln Arg Pro Ser Asp Gly Gln Trp Gly Leu Gln Val Cys
            340             345             350

tgaatgccat gaagacaaat ggcccagcag caaagcagag acctgggcaa ctgtgagtta  1477

aatctgaagg gtgagggact tgaaaaatga cagcccccccc ccccgcccca cccgcccgcc  1537

cgccccgctc tttctcagct gtgtctttct cactcaagta gaagcaaaat ctaaaaaaaa  1597
```

FIG. 3C

```
aaaaaaaaaa aaaaaaaaaa agggcggccg ctctagagga tccaagctta cgtacgcgtg 1657

catgcgacgt c                                                          1668
```

FIG. 4

```
                                        TM1
hu_GPCR    1         MYNGSCCRIEGDTIS QVMPPLLIVAFVLGALGNGVALCGFCF  42
mu_GPCR    1  MPVLSPTAMDNGSCCLIEGEPIS QVMPPLLILVFVLGALGNGIALCGFCF  50
ra_GPCR    1  MLFLSPSAMDNGSCCLIEGEPIT QVMPPLLILAFLLGALGNGLALCGFCF  50
              *  ***** ***. *.*******. *.*******.*******

                        TM2            extracellular loop 1
hu_GPCR   43  HMKTWKPST VYLFNLAVADFLLMICLPFRTDYYLRRRHWAFGDIPCRV GL   92
mu_GPCR   51  HMKTWKSST TIYLFNLAVADFLLMICLPLRTDYYLRRRHWIFGDIACRL VL  100
ra_GPCR   51  HMKTWKSST TIYLFNLAVADFLLMICLPLRTDYYLRRRHWILGDIPCRL VL  100
              ****** **.****************** ***********  *** **. *

            TM3                                    TM4
hu_GPCR   93  FTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLWAL 142
mu_GPCR  101  FKLAMNRAGSIVFLTVVAVDRYFKVVHPHHMVNAISNRTAAATACVLWTL 150
ra_GPCR  101  FMLAMNRAGSIVFLTVVAVDRYFKVVHPHHMVNAISNRTAAAIVCVLWTL 150
              * ****************** ********** **.**.* **   * **.*

                    extracellular loop 2           TM5
hu_GPCR  143  VILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGII 192
mu_GPCR  151  VILGTVYLLMESHLCVQGTLSSCESFIMESANGWHDVMFQLEFFLPLTII 200
ra_GPCR  151  VILGTVYLLMESHLCVRGMVSSCESFIMESANGWHDIMFQLEFFLPLTII 200
              *********.* ****.      ***************.*******.** **

                                            TM6
hu_GPCR  193  LFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLY 242
mu_GPCR  201  LFCSVNVVWSLRRRQQLTRQARMRRATRFIMVVASVFITCYLPSVLARLY 250
ra_GPCR  201  LFCSFKVVWSLRQRQQLTRQARMRRATRFIMVVASVFITCYLPSVLARLY 250
              ****  .*****.****.*****..********* ********** ****

             extracellular
               loop 3            TM7
hu_GPCR  243  FLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
mu_GPCR  251  FLWTVPTSACDPSVHTALHVTLSFTYLNSMLDPLVYYFSSPSLPKFYAKL 300
ra_GPCR  251  FLWTVPSSACDPSVHIALHVTLSLTYLNSMLDPLVYYFSSPSFPKFYAKL 300
              ******.******** ***.*** **.***************** **** **

hu_GPCR  293  KICSLKPKQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHI 342
mu_GPCR  301  TICSLKPKRPGRTKTRRSEEMPISNLCSKSSIDGANRSQRPSDGQWDLQV 350
ra_GPCR  301  KIRSLKPRRPGRSQARRSEEMPISNLCRKSSTDVVNSSQRPSDGQWGLQV 350
              * ****..**.....* ******** .*.   *  *  *****  ..

hu_GPCR  343  VEWH 346
mu_GPCR  351  C    351
ra_GPCR  351  C    351
```

FIG. 5